

CR	MitoCR	RS000056016V01	complete	9	RSA001145133	578	TGTA AACGACGGCCAGTCTAGGAGGGCTCTTGGCCCT	CAGGAAACAGCTATGACCGGGTTGATGTGGTTGGTT	H2	34	MT	16658	17236	-70	508
CR	MitoCR	RS000056016V01	complete	9	RSA001250252	589	TGTA AACGACGGCCAGTGA AAAAGTCTTTAACTCCACCATTAGCAC	CAGGAAACAGCTATGACCGGGAACGTGTGGCTATTTAGGCT	H1	34	MT	17011	17600	283	872
CR	MitoCR	RS000056016V01	complete	9	RSA001250249	548	TGTA AACGACGGCCAGTCTCCACCATTAGCACCCAAAGCT	CAGGAAACAGCTATGACCTGGCCCTGAAGTAGGAACACA	H1	34	MT	17025	17573	297	945
CR	MitoCR	RS000056016V01	complete	9	RSA001308206	574	TGTA AACGACGGCCAGTCGGTACCATAAATCTTGACCACCTGTAGTAC	CAGGAAACAGCTATGACCGACAGATACTGCGACATAGGGTGT	H1	34	MT	17179	17753	451	1025
CR	MitoCR	RS000056016V01	complete	9	RSA001250250	656	TGTA AACGACGGCCAGTCCCCCATGCTTACAAGCAAGT	CAGGAAACAGCTATGACCCGTGTGGAAGCGGCTGTG	H2	34	MT	17240	17896	512	1168
CR	MitoCR	RS000056016V01	complete	9	RSA001250240	575	TGTA AACGACGGCCAGTCCGACATCTGGTTCCTACTTCAGG	CAGGAAACAGCTATGACCGGGTTGATTTGATGAGATTAGTAGTATGGGAG	M	34	MT	17544	18119	816	1391
CR	MitoCR	RS000056016V01	complete	9	RSA001145161	493	TGTA AACGACGGCCAGTCAGGTCTATCACCTATTACCACCTCACG	CAGGAAACAGCTATGACCGGGTTGATTTGATGAGATTAGTAGTATGGGAG	H2	34	MT	17626	18119	898	1391
CR	MitoCR	RS000056016V01	complete	9	RSA001145116	599	TGTA AACGACGGCCAGTTGGCCACAGCACTTAACACATCTC	CAGGAAACAGCTATGACCTTGGTTAATCGTGTGCCGCG	H2	34	MT	17943	18542	1215	1814
CR	MitoCR	RS000056016V01	complete	9	RSA001250241	607	TGTA AACGACGGCCAGTTGGCCACAGCACTTAACACATCTC	CAGGAAACAGCTATGACCCATTGACTTGGTTAATCGTGTGACC	H2	34	MT	17943	18550	1215	1822